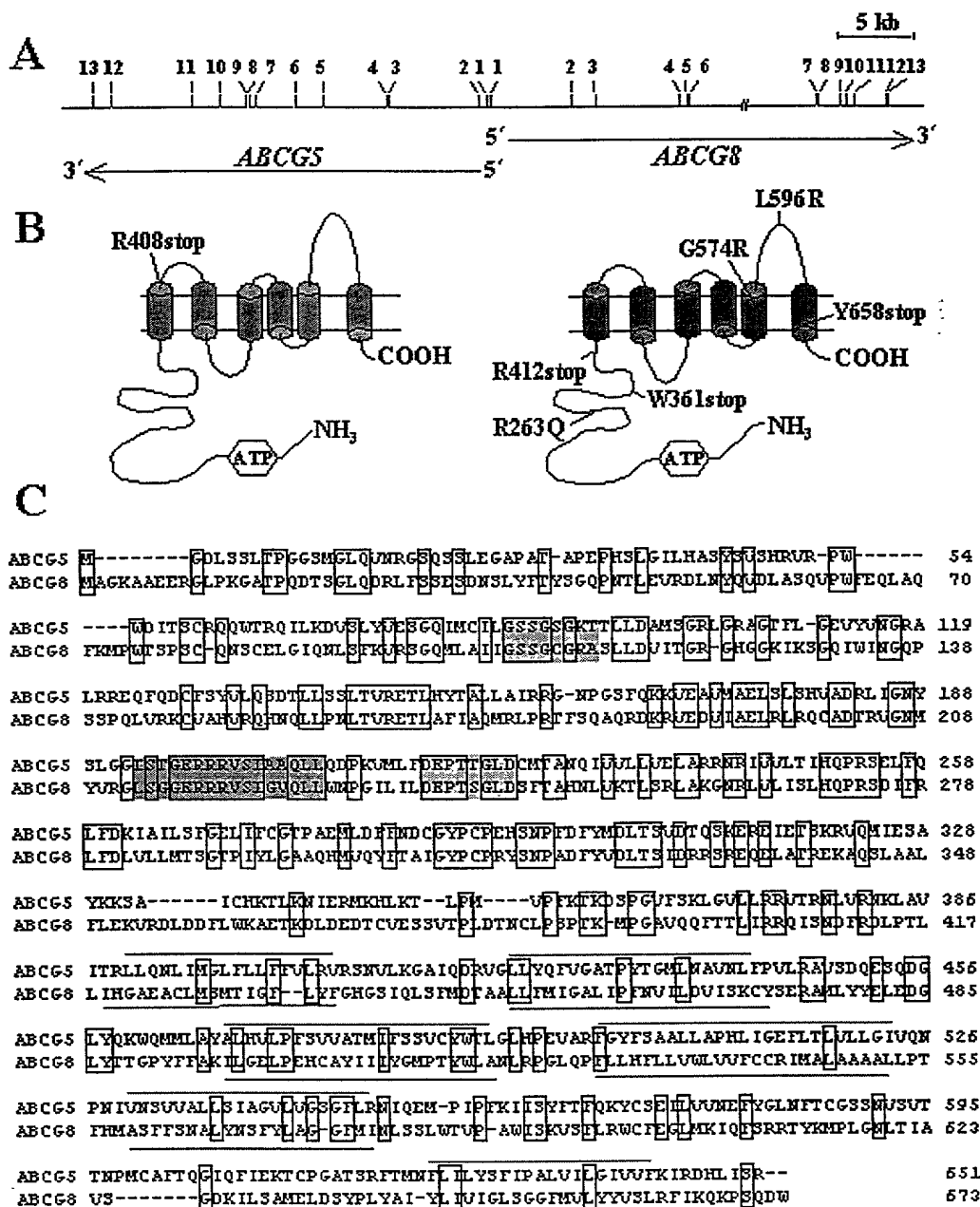
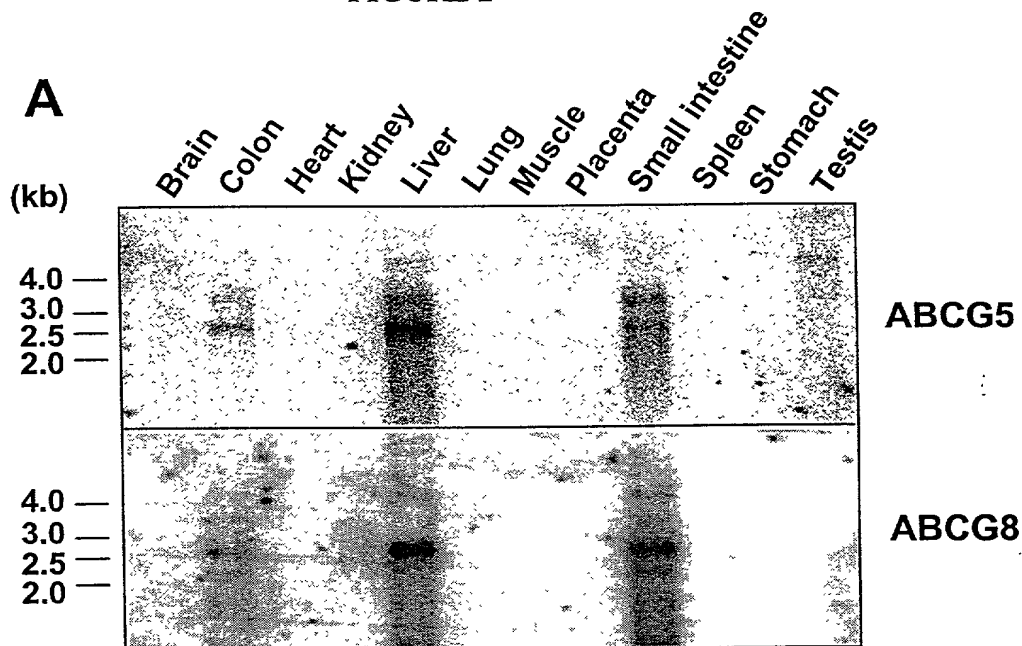


FIGURE 1



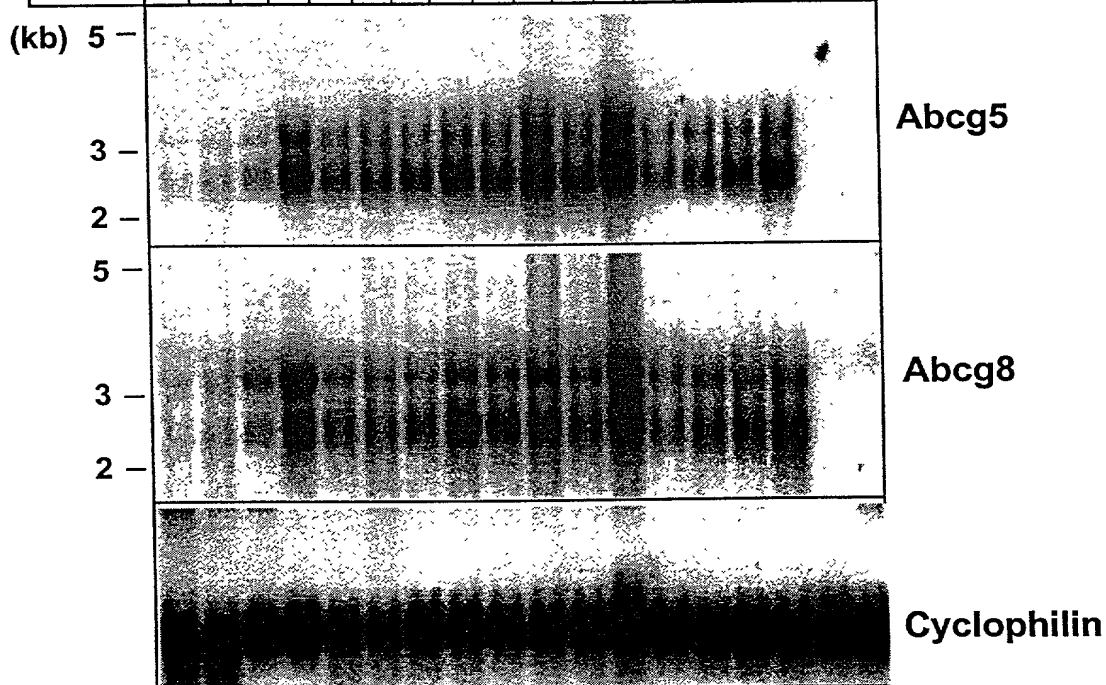
FOO2T-18668660

FIGURE 2



**B**

| Tissue | Liver |   |   |   | Duodenum |   |   |   | Jejunum |   |   |   | Ileum |   |   |   | Kid. |   |
|--------|-------|---|---|---|----------|---|---|---|---------|---|---|---|-------|---|---|---|------|---|
| Day    | 1     |   | 7 |   | 1        |   | 7 |   | 1       |   | 7 |   | 1     |   | 7 |   | 7    |   |
| Chol.  | -     | + | - | + | -        | + | - | + | -       | + | - | + | -     | + | - | + | -    | + |



A. *ABCG8* exon 2 (reverse strand) thru *ABCG5* exon 2 (forward strand)

[illegible]

### FIGURE 3 (CONTINUED)

gcccccaattctactttcaactgatattccacatctggaaagttttgtcaaggagttgtaggcaggacttaacttct  
attcctgaccctacttgtcttttcattatgatggcatcagacacacagttgagaacagataccactaaaaagacctca  
tgtaatatagttctaccgagcacaccaagcacaccaggtttctttgggcctctctcttcaggagttaaagcatcacaca  
cactgcgctgagcccacctgtgtgtattccccgtgtctcactattctttccaggtgagattttaacctttgaatgtgact  
tccatgtttgtttgtgttcttccactaactgtcattatcctctgaggggtttcctcctctgccccctgcaaacctatag  
ctgtaaattttcctatctgcagcagctggggaggggtacactggcccagaagaggggctctgggtagcatgccgcagtg  
tcgcaacactgggttattctgaatgcctctgttaaggattctggcatattcgactcacagaccgttcttgactgagcag  
cccttgtaaaactgtcagcatttaactgtcccttgctgtctcttagaaacaggcagtgtaaggctgtggggaga  
gtcaggtatgacactgttgggtgtagctgagagtgaagtcctcaa

The 4 exons are underlined and the conserved regions are in uppercase. The sequence ends in intron 2 of ABCG5 and is in the following order:

ABCG8      exon 2      (reverse strand)  
ABCG8      intron 1    (reverse strand)  
ABCG8      exon 1      (reverse strand)

gap between genes

ABCG5      exon 1      (forward strand)  
ABCG5      intron 1    (forward strand)  
ABCG5      exon 2      (forward strand)  
ABCG5      intron 2    (forward strand, partial)

#### B. Sequence Between ABCG5 and ABCG8 Containing the Control Sequences

gaccagtgcgtgtttgtgccctttgtgtggcctccctgctgttgggctctctctgtctttgtccttagagctggggcacctgagccctcctc  
tgtgccagccttTCTCCAGCATTCTCTTCTGGCAAACACTTCCTATAAACACACCGTGTGTTCTGCCTATTGTCGAGATAAGGACACTCTGG  
CTAAAGGTACATCAGATAATGGCATCGTTGGCCAAatttggtgaactgttatctcacgaggattccagggtgggttaggatcgacagggcact  
ccattggctcctcagttaaaagctgccctggagccggacaggccactagaaaattcattgcatttgcttctctgctagcc

SF 1157042 v1

09393931 112001  
T02011 135350